

Supplementary Table 1. UniProt Accession numbers for the reference sequences in the analysis

Pathway	Abbreviation	Description of Protein	UniProt-ID
Fatty Acid Synthesis-I	<i>fas</i>	3-oxoacyl-ACP synthase	P95029(MT), Q8NS46(CG)
Fatty Acid Synthesis-II	<i>fabD</i>	Malonyl CoA-acyl carrier protein transacylase	P9WNG5(MT)
	<i>fabH</i>	3-oxoacyl-[acyl-carrier-protein] synthase 3	P9WNG3(MT)
	<i>kasA</i>	3-oxoacyl-[acyl-carrier-protein] synthase 1	P9WQD9(MT)
	<i>kasB</i>	3-oxoacyl-[acyl-carrier-protein] synthase 2	P9WQD7(MT)
	<i>mabA</i>	3-oxoacyl-[acyl-carrier-protein] reductase	P9WGT3(MT)
	<i>hadA</i>	(3R)-hydroxyacyl-ACP dehydratase subunit HadA	P9WFK1(MT)
	<i>hadB</i>	(3R)-hydroxyacyl-ACP dehydratase subunit HadB	I6WYY7(MT)
	<i>hadC</i>	(3R)-hydroxyacyl-ACP dehydratase subunit HadC	P9WEJ9(MT)
Mycolic Acid Biosynthesis: Carboxylation	<i>inhA</i>	Enoyl-[acyl-carrier-protein] reductase	P9WGR1(MT)
	<i>accD6</i>	Acetyl-CoA carboxylase beta subunit	P9WQH5(MT)
	<i>accD4</i>	Acyl-CoA carboxylase subunit beta 1	Q53578(MT)
	<i>accD5</i>	Acyl-CoA carboxylase subunit beta 2	P9WQH7(MT)
	<i>accA3</i>	Acyl/Acetyl-CoA carboxylase subunit alpha	P96890(MT)
Mycolic Acid Biosynthesis: Condensation	<i>accE</i>	Acyl/Acetyl-CoA carboxylase subunit epsilon	P96886(MT)
	<i>pks13</i>	Polyketide synthase	I6X8D2(MT), Q8NLR7(CG)
Mycolic Acid Biosynthesis: Activation	<i>fadD32</i>	Long-chain-fatty-acid--AMP ligase	Q53580(MT), Q8NLR6(CG)
Mycolic Acid Biosynthesis: Reduction	<i>cmrA</i>	Probable short-chain type dehydrogenase/reductase	I6Y9I3(MT), Q8NMU2(CG)
Mycolic Acid Biosynthesis: Transport	<i>mmpL3</i>	Trehalose monomycolate exporter	P9WJV5(MT), Q8NLS1(CG)
Mycolic Acid Cyclization, Methylation	<i>cmaA1</i>	Cyclopropane mycolic acid synthase 1	P9WPB7(MT)
	<i>cmaA2</i>	Cyclopropane mycolic acid synthase 2	P9WPB5(MT)
	<i>umaA1</i>	Possible mycolic acid synthase	Q6MX39(MT)
	<i>pcaA</i>	Cyclopropane mycolic acid synthase 3	P9WPB3(MT)
	<i>mmaA1</i>	Mycolic acid methyltransferase	P9WPB1(MT)
	<i>mmaA2</i>	Cyclopropane mycolic acid synthase	Q79FX6(MT)
	<i>mmaA3</i>	Methoxy mycolic acid synthase	P0CH91(MT)
	<i>mmaA4</i>	Hydroxymycolate synthase	Q79FX8(MT)
Mycolic Acid Desaturation	<i>desA1</i>	Putative acyl-desaturase	P9WNZ7(MT)
	<i>desA2</i>	Putative acyl-desaturase	P9WNZ5(MT)
	<i>desA3</i>	NADPH-dependent stearyl-CoA 9-desaturase	P9WNZ3(MT)
Menaquinone Biosynthesis Pathway: Classical	<i>menA</i>	1,4-dihydroxy-2-naphthoate octaprenyltransferase	P9WIP3(MT)
	<i>menB</i>	1,4-dihydroxy-2-naphthoyl-CoA synthase	P9WNP5(MT)
	<i>menC</i>	o-succinylbenzoate synthase	P9WJP3(MT)
	<i>menD</i>	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase	P9WK11(MT)
	<i>menE</i>	2-succinylbenzoate--CoA ligase	P9WQ39(MT)
	<i>menF</i>	Isochorismate synthase	P9WFW9(MT)
	<i>menG</i>	Demethylmenaquinone methyltransferase	P9WFR3(MT)
Menaquinone Biosynthesis Pathway: Fetalosine	<i>mqnA</i>	Chorismate dehydratase	Q9L0T8(SCO), A1W0R9(CJ), Q5SK49(TT)
	<i>mqnB</i>	Fetalosine hydrolase	Q9KXN0(SCO), Q5SKT7(TT), A0LR22(ACE)
	<i>mqnC</i>	Cyclic dehydropantidine fetalosine synthase	Q9XAP2(SCO), Q9K864(BH)
	<i>mqnD</i>	1,4-dihydroxy-6-naphthoate synthase	Q9KXN1(SCO), Q5SI12(TT)
	<i>mqnE</i>	Aminodeoxyfetalosine synthase	Q8CJT5(SCO), Q5SK48(TT)
	SCO4490	Putative decarboxylase	Q9KYP3(SCO)
	SCO4491	Putative octaprenyltransferase	Q9KYP2(SCO)
	<i>ubiX</i>	Flavin prenyltransferase	Q9KYP1(SCO)
Menaquinone Isoprenyl Chain Elongation	<i>uppS</i>	Decaprenyl diphosphate synthase	P9WFF7(MT)
	<i>hepST</i>	Geranylgeranyl pyrophosphate synthase	Q8NT37(CG)
Menaquinone Isoprenyl Chain Saturation	<i>menJ</i>	Menaquinone reductase	P9WNY9(MT)